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RAW SEQUENCE LISTING

DATE: 04/02/2002

PATENT APPLICATION: US/09/856,796A

TIME: 08:32:39

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3 <110> APPLICANT: HIRSCH, FRANCOIS
4   HAEFFNER, ASTRID
6 <120> TITLE OF INVENTION: NF-KB ACTIVATION INHIBITORS, AND THEIR PHARMACEUTICAL
7   USES
9 <130> FILE REFERENCE: USB98CNRN
11 <140> CURRENT APPLICATION NUMBER: 09/856,796A
12 <141> CURRENT FILING DATE: 2001-05-25
14 <150> PRIOR APPLICATION NUMBER: PCT/FR99/02897
15 <151> PRIOR FILING DATE: 1999-11-24
17 <150> PRIOR APPLICATION NUMBER: FR 98/14858
18 <151> PRIOR FILING DATE: 1998-11-25
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <211> LENGTH: 609
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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31 <222> LOCATION: (1)..(606)
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36   1               5               10               15
38 tgc ctg ccc tgg ctt caa gag ggc agt gcc ttc cca acc att ccc tta      96
39 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
40   20               25               30
42 tcc agg ctt ttt gac aac gct agt ctc cgc gcc cat cgt ctg cac cag      144
43 Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu His Gln
44   35               40               45
46 ctg gcc ttt gac acc tac cag gag ttt aac ccc cag acc tcc ctc tgt      192
47 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Asn Pro Gln Thr Ser Leu Cys
48   50               55               60
50 ttc tca gag tct att ccg aca ccc tcc aac agg gag gaa aca caa cag      240
51 Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln
52  65               70               75               80
54 aaa tcc aac cta gag ctg ctc cgc atc tcc ctg ctg ctc atc cag tcg      288
55 Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser
56   85               90               95
58 tgg ctg gag ccc gtg cag ttc ctc agg agt gtc ttc gcc aac agc ctg      336
59 Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu
60  100              105              110
62 gtg tac ggc gcc tct gac agc aac gtc tat gac ctc cta aag gac cta      384

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63 Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu
64      115      120      125
66 gag gaa ggc atc caa acg ctg atg ggg agg ctg gaa gat ggc agc ccc 432
67 Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro
68      130      135      140
70 cgg act ggg cag atc ttc aag cag acc tac agc aag ttc gac aca aac 480
71 Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn
72 145      150      155      160
74 tca cac aac gat gac gca cta ctc aag aac tac ggg ctg ctc tac tgc 528
75 Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys
76      165      170      175
78 ttc agg aag gac atg gac aag gtc gag aca ttc ctg cgc atc gtg cag 576
79 Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln
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96 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
97      20      25      30
99 Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu His Gln
100      35      40      45
102 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Asn Pro Gln Thr Ser Leu Cys
103      50      55      60
105 Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln
106 65      70      75      80
108 Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser
109      85      90      95
111 Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu
112      100      105      110
114 Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu
115      115      120      125
117 Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro
118      130      135      140
120 Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn
121 145      150      155      160
123 Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys
124      165      170      175
126 Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln
127      180      185      190
129 Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
130      195      200
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145 1 5 10 15
147 ctg tcg ctc cct ctg ggc ctc cca gtc ctg ggc gcc cca cca cgc ctc 96
148 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
149 20 25 30
151 atc tgt gac agc cga gtc ctg gag agg tac ctc ttg gag gcc aag gag 144
152 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
153 35 40 45
155 gcc gag aat atc acg acg ggc tgt gct gaa cac tgc agc ttg aat gag 192
156 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
157 50 55 60
159 aat atc act gtc cca gac acc aaa gtt aat ttc tat gcc tgg aag agg 240
160 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
161 65 70 75 80
163 atg gag gtc ggg cag cag gcc gta gaa gtc tgg cag ggc ctg gcc ctg 288
164 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
165 85 90 95
167 ctg tcg gaa gct gtc ctg cgg ggc cag gcc ctg ttg gtc aac tct tcc 336
168 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
169 100 105 110
171 cag ccg tgg gag ccc ctg cag ctg cat gtg gat aaa gcc gtc agt ggc 384
172 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
173 115 120 125
175 ctt cgc agc ctc acc act ctg ctt cgg gct ctg gga gcc cag aag gaa 432
176 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
177 130 135 140
179 gcc atc tcc cct cca gat gcg gcc tca gct gct cca ctc cga aca atc 480
180 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
181 145 150 155 160
183 act gct gac act ttc cgc aaa ctc ttc cga gtc tac tcc aat ttc ctc 528
184 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
185 165 170 175
187 cgg gga aag ctg aag ctg tac aca ggg gag gcc tgc agg aca ggg gac 576
188 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
189 180 185 190
191 aga tga 582
192 Arg
195 <210> SEQ ID NO: 4
196 <211> LENGTH: 193
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens

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204 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
205           20           25           30
207 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
208           35           40           45
210 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
211           50           55           60
213 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
214   65           70           75           80
216 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
217           85           90           95
219 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
220           100          105          110
222 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
223           115          120          125
225 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
226           130          135          140
228 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
229 145           150          155          160
231 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
232           165          170          175
234 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
235           180          185          190
237 Arg

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VERIFICATION SUMMARY

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